



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,067

DATE: 02/13/2002

TIME: 12:54:10

Input Set : A:\SEQUENCE LISTIN1.txt

Output Set: N:\CRF3\02132002\I647067.raw

RECEIVED

MAR 14 2002

TECH CENTER 1600/2900

ENTERED

4 <110> APPLICANT: Hsueh, Aaron J. W.  
5 Hsu, Sheau Yu  
6 Liang, Shan-Guang  
7 Van Der Spek, Petrus Johannes  
9 <120> TITLE OF INVENTION: Novel Mammalian G-Protein Coupled  
10 Receptors Having Extracellular Leucine Rich Repeat Regions  
13 <130> FILE REFERENCE: STAN-084  
15 <140> CURRENT APPLICATION NUMBER: 09/647,067  
16 <141> CURRENT FILING DATE: 2000-09-25  
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/06573  
19 <151> PRIOR FILING DATE: 1999-03-25  
21 <150> PRIOR APPLICATION NUMBER: 60/079,501  
22 <151> PRIOR FILING DATE: 1998-03-26  
24 <160> NUMBER OF SEQ ID NOS: 8  
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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29 <211> LENGTH: 2856  
30 <212> TYPE: DNA  
31 <213> ORGANISM: homo sapiens  
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36 gtggactgct ccggaaagg gttgacggcc gtaccggagg gtctcagcgc cttcacccaa 180  
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38 ccatttctag aggagctaca actggctggt aacgaccttt ctcttatcca tccaaaagcc 300  
39 ttgtctgggc tgaagaact caaagtccta acactccaga ataatcagtt gagaacagtg 360  
40 ccagtgaaag ccattcacgg actgagtgtc ttgcagttct tacgcttaga tgccaacct 420  
41 attacctcag tcccggagga cagttttgaa gggcttgtcc agttacgcca tctgtggctg 480  
42 gatgacaaca gcttgacgga agtgcccgty cgtccctca gcaacctgcc aacctgcag 540  
43 gcgtgacct tggctctcaa caacatctca agcatccctg acttcgcttt caccaacctt 600  
44 tcaagcttgg tggttctgca tctgcataac aataaaatta aaagcctcag tcaacactgt 660  
45 tttgatggac tagataacct ggaaaccttg gacttgaatt acaattactt ggatgagttt 720  
46 cctcaggcta ttaaagccct tcccagcctt aaagagctgg gatttcacag taattctatt 780  
47 tctgttattc ctgatggagc atttggtggt aatccactgc taagaactat tcatttgtat 840  
48 gataatcctc tgtcttttgt ggggaactca gcatttcaca acctgtctga tctgcattgc 900  
49 ttagtcattc gtggtgcaag cctggtgcag tggttcccca atctgaccgg aactgtccat 960  
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51 aacaaaaaga tgcagaggac tctggactta tcttataaca atataagaga ccttccaagt 1080  
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53 aaggaaaata cttttcaagg cctaacatct ctaaggattc tagatctgag tagaaacctg 1200  
54 atccgtgaaa ttcacagtgg agcttttgcg aagcttggga caattactaa cctggatgta 1260  
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56 cttgtgggta acttcaagct gaaagacgcc ttggcagcca gagactttgc taatctcagg 1380

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57 tctctatcag taccatatgc ttatcagtgt tgtgcatttt gggggtgtga ctctttatgc 1440
58 aaattaaaca cagaagataa cagcccccac gaacacagtg tgacaaaaga gaaaggtgct 1500
59 acagatgcag caaatgtcac cagcactgct gagaacgaag aacatagcca aataattatc 1560
60 cactgtacac cttcaacagg tgctttcaag ccctgtgaat atttactggg aagctggatg 1620
61 attgcctta cagtgtggtt cattttcctg gtgccttgc ttttcaacct gcttgtcatt 1680
62 ttaacagtgt ttgcgtcttg ttcactactg cctgcctcca aactcttcat aggcttgatt 1740
63 tctgtgtcta acttactcat gggcatctat actggcatcc ttacttttct tgatgctgtg 1800
64 tcctggggcc gatttgccga atttggcatt tgggtggaaa ctggcagcgg ctgcaaggta 1860
65 gccgggtctc tggcagtctt ctccctcagag agcgtgtgat tcctattaac actggcagct 1920
66 gtggaaagaa gcgtatttgc aaaggatttg atgaaacacg ggaagagcag tcacctcaga 1980
67 cagttccagg tggccgccct cttagctttg ctgggtgccg cagtggcagg ctgcttcccc 2040
68 cttttccacg gagggaataa ttctgcacgc cccttgtgtt tgccgtttcc tacaggagaa 2100
69 accccatcgt taggattcac tgtgacctta gtgctattaa actcactggc atttttacta 2160
70 atggccatta tctacactaa actatactgc aacttagaga aggaggacct gtcggaaaac 2220
71 tcccagtcta gcgtgattaa gcacgttgcc tggctcatct tcacaaactg catcttcttc 2280
72 tgccctgttg catttttctc atttgcacca ttgatcacgg caatctocat cagccccgag 2340
73 ataataagat ctgttacact gatattcttc ccgttgctg cttgcctgaa tccggctctg 2400
74 tatgttttct tcaacccaaa gtttaaagaa gactggaagc tactgaagcg gcgtgttacc 2460
75 aggaacacg gatctgtttc agtttccatc agcagccaag gcggttgtgg ggaacaggat 2520
76 ttctactatg actgtggcat gtattccac ttgcagggtg acctgactgt ctgtgactgc 2580
77 tgtgagtcat ttcttttgac aaaaccagta tcatgcaaac acttaataaa atgcacagt 2640
78 tgtcctgtat tgacagcggc ctcttgccag aggccagagg cctactggtc tgattgtggt 2700
79 acacagtcag ccattctga ctatgcagat gaagaagatt cctttgtctc agacagctct 2760
80 gaccaggtgc aggcctgtgg acgagcctgc ttctaccaga gtcgtggatt ccctctggtg 2820
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83 &lt;210&gt; SEQ ID NO: 2

84 &lt;211&gt; LENGTH: 951

85 &lt;212&gt; TYPE: PRT

86 &lt;213&gt; ORGANISM: human

88 &lt;400&gt; SEQUENCE: 2

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90 1 5 10 15
91 Gly Ser Ala Gly Pro Ser Gly Ala Ala Pro Pro Leu Cys Ala Ala Pro
92 20 25 30
93 Cys Ser Cys Asp Gly Asp Arg Arg Val Asp Cys Ser Gly Lys Gly Leu
94 35 40 45
95 Thr Ala Val Pro Glu Gly Leu Ser Ala Phe Thr Gln Ala Leu Asp Ile
96 50 55 60
97 Ser Met Asn Asn Ile Thr Gln Leu Pro Glu Asp Ala Phe Lys Ser Phe
98 65 70 75 80
99 Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Leu Ile
100 85 90 95
101 His Pro Lys Ala Leu Ser Gly Leu Lys Glu Leu Lys Val Leu Thr Leu
102 100 105 110
103 Gln Asn Asn Gln Leu Arg Thr Val Pro Ser Glu Ala Ile His Gly Leu
104 115 120 125
105 Ser Ala Leu Gln Ser Leu Arg Leu Asp Ala Asn His Ile Thr Ser Val
106 130 135 140
107 Pro Glu Asp Ser Phe Glu Gly Leu Val Gln Leu Arg His Leu Trp Leu

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```

108 145          150          155          160
109 Asp Asp Asn Ser Leu Thr Glu Val Pro Val Arg Pro Leu Ser Asn Leu
110          165          170          175
111 Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Asn Ile Ser Ser Ile
112          180          185          190
113 Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu
114          195          200          205
115 His Asn Asn Lys Ile Lys Ser Leu Ser Gln His Cys Phe Asp Gly Leu
116          210          215          220
117 Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Tyr Leu Asp Glu Phe
118 225          230          235          240
119 Pro Gln Ala Ile Lys Ala Leu Pro Ser Leu Lys Glu Leu Gly Phe His
120          245          250          255
121 Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Gly Gly Asn Pro
122          260          265          270
123 Leu Leu Arg Thr Ile His Leu Tyr Asp Asn Pro Leu Ser Phe Val Gly
124          275          280          285
125 Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Cys Leu Val Ile Arg
126          290          295          300
127 Gly Ala Ser Leu Val Gln Trp Phe Pro Asn Leu Thr Gly Thr Val His
128 305          310          315          320
129 Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asp
130          325          330          335
131 Asp Leu Cys Gln Asn Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr
132          340          345          350
133 Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys Arg Ala Leu Glu
134          355          360          365
135 Glu Ile Ser Leu Gln Arg Asn Gln Ile Ser Leu Ile Lys Glu Asn Thr
136          370          375          380
137 Phe Gln Gly Leu Thr Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu
138 385          390          395          400
139 Ile Arg Glu Ile His Ser Gly Ala Phe Ala Lys Leu Gly Thr Ile Thr
140          405          410          415
141 Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly
142          420          425          430
143 Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys
144          435          440          445
145 Asp Ala Leu Ala Ala Arg Asp Phe Ala Asn Leu Arg Ser Leu Ser Val
146          450          455          460
147 Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Trp Gly Cys Asp Ser Leu Cys
148 465          470          475          480
149 Lys Leu Asn Thr Glu Asp Asn Ser Pro Gln Glu His Ser Val Thr Lys
150          485          490          495
151 Glu Lys Gly Ala Thr Asp Ala Ala Asn Val Thr Ser Thr Ala Glu Asn
152          500          505          510
153 Glu Glu His Ser Gln Ile Ile Ile His Cys Thr Pro Ser Thr Gly Ala
154          515          520          525
155 Phe Lys Pro Cys Glu Tyr Leu Leu Gly Ser Trp Met Ile Arg Leu Thr
156          530          535          540

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157 Val Trp Phe Ile Phe Leu Val Ala Leu Leu Phe Asn Leu Leu Val Ile
158 545 550 555 560
159 Leu Thr Val Phe Ala Ser Cys Ser Ser Leu Pro Ala Ser Lys Leu Phe
160 565 570 575
161 Ile Gly Leu Ile Ser Val Ser Asn Leu Leu Met Gly Ile Tyr Thr Gly
162 580 585 590
163 Ile Leu Thr Phe Leu Asp Ala Val Ser Trp Gly Arg Phe Ala Glu Phe
164 595 600 605
165 Gly Ile Trp Trp Glu Thr Gly Ser Gly Cys Lys Val Ala Gly Ser Leu
166 610 615 620
167 Ala Val Phe Ser Ser Glu Ser Ala Val Phe Leu Leu Thr Leu Ala Ala
168 625 630 635 640
169 Val Glu Arg Ser Val Phe Ala Lys Asp Leu Met Lys His Gly Lys Ser
170 645 650 655
171 Ser His Leu Arg Gln Phe Gln Val Ala Ala Leu Leu Ala Leu Leu Gly
172 660 665 670
173 Ala Ala Val Ala Gly Cys Phe Pro Leu Phe His Gly Gly Gln Tyr Ser
174 675 680 685
175 Ala Ser Pro Leu Cys Leu Pro Phe Pro Thr Gly Glu Thr Pro Ser Leu
176 690 695 700
177 Gly Phe Thr Val Thr Leu Val Leu Leu Asn Ser Leu Ala Phe Leu Leu
178 705 710 715 720
179 Met Ala Ile Ile Tyr Thr Lys Leu Tyr Cys Asn Leu Glu Lys Glu Asp
180 725 730 735
181 Leu Ser Glu Asn Ser Gln Ser Ser Val Ile Lys His Val Ala Trp Leu
182 740 745 750
183 Ile Phe Thr Asn Cys Ile Phe Phe Cys Pro Val Ala Phe Phe Ser Phe
184 755 760 765
185 Ala Pro Leu Ile Thr Ala Ile Ser Ile Ser Pro Glu Ile Met Lys Ser
186 770 775 780
187 Val Thr Leu Ile Phe Phe Pro Leu Pro Ala Cys Leu Asn Pro Val Leu
188 785 790 795 800
189 Tyr Val Phe Phe Asn Pro Lys Phe Lys Glu Asp Trp Lys Leu Leu Lys
190 805 810 815
191 Arg Arg Val Thr Arg Lys His Gly Ser Val Ser Val Ser Ile Ser Ser
192 820 825 830
193 Gln Gly Gly Cys Gly Glu Gln Asp Phe Tyr Tyr Asp Cys Gly Met Tyr
194 835 840 845
195 Ser His Leu Gln Gly Asn Leu Thr Val Cys Asp Cys Cys Glu Ser Phe
196 850 855 860
197 Leu Leu Thr Lys Pro Val Ser Cys Lys His Leu Ile Lys Ser His Ser
198 865 870 875 880
199 Cys Pro Val Leu Thr Ala Ala Ser Cys Gln Arg Pro Glu Ala Tyr Trp
200 885 890 895
201 Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
202 900 905 910
203 Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
204 915 920 925
205 Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr

```

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```

206      930      935      940
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208 945      950
211 <210> SEQ ID NO: 3
212 <211> LENGTH: 2082
213 <212> TYPE: DNA
214 <213> ORGANISM: homo sapiens
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: 768
219 <223> OTHER INFORMATION: n = A,T,C or G
221 <400> SEQUENCE: 3
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224 acactctcca acttaagga actaggattt catagcaaca atatcagggtc gatacctgag 180
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227 gcctcacaaa taactgaatt tcctgattta actggaactg caaacctgga gagtctgact 360
228 ttaactggag cacagatctc atctcttctt caaacctgtt gcaatcagtt acctaattctc 420
229 caagtgttag atctgtctta caacctatta gaagatttac ccagtttttc agtctgccaa 480
230 aagcttcaga aaattgacct aagacataat gaaatctacg aaattaaagt tgacactttc 540
231 cagcagttgc ttagcctccg atcgtgaat ttggcttgga acaaaattgc tattattcac 600
232 cccaatgcat ttccacttt gccatcccta ataaagctgg acctatcgtc caacctcctg 660
233 tegtcttttc ctataactgg gttacatggt ttaactcact taaaattaac aggaaatcat 720
234 gccttacaga gctggatata atctgaaaac ttccagaaac tcaaggtnat agaaatgcct 780
235 tatgcttacc agtgctgtgc atttggagtg tgtgagaatg cctataagat ttctaataca 840
236 tgggaataaag gtgacaacag cagtatggac gaccttcata agaaagatgc tgggaatgtt 900
237 caggctcaag atgaacgtga ccttgaagat ttctgtcttg actttgagga agacctgaaa 960
238 gcccttcatt cagtgcagtg ttacacctcc ccaggccctt tcaaaccctg tgaacacctg 1020
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241 ttaattgggg tcatcgagc agtgaacatg ctcaaggagg tctccagtc cgtgctggct 1200
242 ggtgtggatg cgttccacttt tggcagcttt gcacgacatg gtgcctgggt ggagaatggg 1260
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245 aaagctccat ttctagcct gaaagtaatc attttgcctt gtgcctgctt ggccttgacc 1440
246 atggccgcag ttccctgct ggggtgcagc aagtatggcg cctccctctt ctgcctgcct 1500
247 ttgccttttg gggagccag caccatgggc tacatggctg ctctcatctt gctcaattcc 1560
248 ctttgccttc tcatgatgac cattgcctac accaagctct actgcaattt ggacaagggg 1620
249 gacctggaga atatttggga ctgctctatg gtaaaacaca ttgcctggtt gctcttcacc 1680
250 aactgcatcc taaactgccc tgtggcttcc ttgtccttct cctctttaat aaaccttaca 1740
251 tttatcagtc ctgaagtaat taagtttata cttctggttg tagtccact tctgcatgt 1800
252 ctcaatcccc ttctctacat cttgttcaat cctcacttta aggaggatct ggtgagcctg 1860
253 agaaagcaaa cctacgtctg gacaagatca aaacacccaa gcttgatgtc aattaactct 1920
254 gatgatgtcg aaaaacagtc ctgtgactca actcaagcct tggtaacctt taccagctcc 1980
255 agcatcactt atgacctgcc tcccagttcc gtgccatcac cagcttatcc agtgactgag 2040
256 agctgccatc ttctctctgt ggcatttgtc ccatgtctct aa 2082
258 <210> SEQ ID NO: 4
259 <211> LENGTH: 693

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTIN1.txt

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L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7